



032301.1181.ST25.txt
SEQUENCE LISTING

RECEIVED

DEC 20 2002

TECH CENTER 1600/2900

*Part of
Paper No. 12*

<110> NAMPOOTHIRI, Madhavan et al.
<120> Nucleotide Sequences which Code for the fadD15 Gene
<130> 032301 WN 1181
<160> 4
<170> PatentIn version 3.1
<210> 1
<211> 2300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (247)..(2103)
<223>

<220>
<221> -10_signal
<222> (95)..(100)
<223>

<220>
<221> -35_signal
<222> (72)..(78)
<223>

<220>
<221> RBS
<222> (188)..(195)
<223>

B'
<400> 1
ttatgccact aatagcgtgt gggcacagca tatttgtagc gtgagggtaa gtttgtaga 60
aaatacatct tttggattgg gctttggggg ggcttttata caccctgatt ggtgcagata 120
taagaagtta ttgacacact gaatacatag agaaaaattc catgtgggta aagatatgcc 180
taaagatctg accaaaaacg tgactaaaga cgtgacgaca caagtacagc caaattaaag 240
gaaagg ttg aat ttg acc atg act tca cct aat acc ctg cag gaa tac 288
Met Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr
1 5 10
act gaa cct gcc aag tac acc atc gga gaa tct gaa acc tgc ctg acc 336
Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr
15 20 25 30
gcc ctt cta gat cag att aag act cga cct tac gga gtt ttg ttc agc 384
Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser
35 40 45
aag cct gcc aac tat gag tgg gtg aat gta act gcc aaa gaa ttt cag 432
Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln
50 55 60
gac gag gtt ttt gcg gtt gca aaa gga att att tca gtc ggc gta gag 480

Asp	Glu	Val	Phe	Ala	Val	Ala	Lys	Gly	Ile	Ile	Ser	Val	Gly	Val	Glu		
		65					70					75					
cag	gga	gac	cgt	gtc	gcg	ctg	ctg	tcc	aat	act	cgc	tat	gag	tgg	gct	528	
Gln	Gly	Asp	Arg	Val	Ala	Leu	Leu	Ser	Asn	Thr	Arg	Tyr	Glu	Trp	Ala		
	80					85					90						
gtg	ctt	gat	ttc	gct	atc	tgg	gcc	gct	ggc	gca	gtg	agc	gtg	cct	atc	576	
Val	Leu	Asp	Phe	Ala	Ile	Trp	Ala	Ala	Gly	Ala	Val	Ser	Val	Pro	Ile		
	95				100					105					110		
tac	agc	tcc	tct	tca	ctg	tcc	caa	att	gag	tgg	atc	att	gag	gat	tcc	624	
Tyr	Ser	Ser	Ser	Ser	Leu	Ser	Gln	Ile	Glu	Trp	Ile	Ile	Glu	Asp	Ser		
				115					120					125			
ggc	gct	gtt	ttg	gcc	att	acc	gaa	acc	cct	gat	cat	acc	gac	ttg	atg	672	
Gly	Ala	Val	Leu	Ala	Ile	Thr	Glu	Thr	Pro	Asp	His	Thr	Asp	Leu	Met		
			130					135					140				
aag	aac	ctg	gtc	atc	ggc	gaa	gac	gga	act	cca	gcg	att	aag	ggt	tca	720	
Lys	Asn	Leu	Val	Ile	Gly	Glu	Asp	Gly	Thr	Pro	Ala	Ile	Lys	Gly	Ser		
		145					150					155					
cct	tcc	aag	ctg	cg	cg	att	cta	gag	atc	aac	tct	tcg	gcg	ttg	gag	768	
Pro	Ser	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ile	Asn	Ser	Ser	Ala	Leu	Glu		
	160					165					170						
acc	ttg	aag	ttt	gag	ggc	cg	gag	ctt	tct	gat	gag	ctg	gtg	tgg	gaa	816	
Thr	Leu	Lys	Phe	Glu	Gly	Arg	Glu	Leu	Ser	Asp	Glu	Leu	Val	Trp	Glu		
	175				180					185					190		
cg	att	cat	gca	acc	aag	gcc	gct	gac	ctg	gcg	tct	ttg	gtg	tac	acc	864	
Arg	Ile	His	Ala	Thr	Lys	Ala	Ala	Asp	Leu	Ala	Ser	Leu	Val	Tyr	Thr		
				195					200					205			
tct	ggc	aca	act	ggc	agg	ccg	aag	ggc	tgc	gag	ttg	tcc	cac	tac	cac	912	
Ser	Gly	Thr	Thr	Gly	Arg	Pro	Lys	Gly	Cys	Glu	Leu	Ser	His	Tyr	His		
			210					215					220				
ttg	ttg	gct	gag	gtc	cga	gcg	ctg	atc	acc	aat	gac	atc	gga	gcg	atc	960	
Trp	Leu	Ala	Glu	Val	Arg	Ala	Leu	Ile	Thr	Asn	Asp	Ile	Gly	Ala	Ile		
		225					230					235					
gcg	atg	cca	ggt	tca	agg	ttg	ctc	acc	ttc	ctt	cct	ttg	gcg	cac	gtt	1008	
Ala	Met	Pro	Gly	Ser	Arg	Leu	Leu	Thr	Phe	Leu	Pro	Leu	Ala	His	Val		
	240					245					250						
ctt	gct	cg	gca	gtg	cac	ttg	gcc	ttc	gct	gtc	acc	ggt	gca	acc	cag	1056	
Leu	Ala	Arg	Ala	Val	His	Leu	Ala	Phe	Ala	Val	Thr	Gly	Ala	Thr	Gln		
	255				260					265					270		
tcc	cac	tgg	tct	gat	ttc	agc	acc	ctt	act	ttg	gaa	ctg	cag	cgt	tcc	1104	
Ser	His	Trp	Ser	Asp	Phe	Ser	Thr	Leu	Thr	Leu	Glu	Leu	Gln	Arg	Ser		
				275					280					285			
cg	ccg	aac	ctg	att	ttg	ggt	gtt	cca	cg	gtg	ttt	gaa	aag	gtc	cg	1152	
Arg	Pro	Asn	Leu	Ile	Leu	Gly	Val	Pro	Arg	Val	Phe	Glu	Lys	Val	Arg		
			290					295					300				
aac	gcc	gct	gct	gct	aat	gct	gct	gac	ggt	ggc	gca	atc	aag	cg	atc	1200	
Asn	Ala	Ala	Ala	Ala	Asn	Ala	Ala	Asp	Gly	Gly	Ala	Ile	Lys	Arg	Ile		
		305					310					315					

032301.1181.ST25.txt

atg ttt gag cgt gcc gaa aag gcg gcc att gaa tac tcc atg gct ctt Met Phe Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu 320 325 330	1248
gat act gca gaa ggc cca agc aag tcc cag gtt atg gca cat aaa gcg Asp Thr Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala 335 340 345 350	1296
ttt gac aag ctg gtg tac tcc aag atc cgt gca gct gtc ggt ggc gat Phe Asp Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp 355 360 365	1344
gtg cag tac gcc atc acc ggt ggt tca gcg atg ggg cag gag ctg ctg Val Gln Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu 370 375 380	1392
cac ttc ttc cgc ggt gtg ggc atg acc atc tac gaa ggt tat ggt ctg His Phe Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu 385 390 395	1440
acg gaa tct gcg gct gct gca gcg gtg gac ttc act gat caa aag atc Thr Glu Ser Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile 400 405 410	1488
ggc act gtg ggt aag ccg atg ggt ggc atg acc atc aag atc aat gaa Gly Thr Val Gly Lys Pro Met Gly Gly Met Thr Thr Ile Lys Ile Asn Glu 415 420 425 430	1536
gat ggc gaa atc atg cta aaa ggc gag atg ttg ttc cag gga tat tgg Asp Gly Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp 435 440 445	1584
aac aac cca gaa gcc aca gca gaa gcc ctc cac gac ggt tgg ttc aac Asn Asn Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn 450 455 460	1632
acc ggc gat ctg ggt gag ctg ttg gag tct gga cac ctg gtg atc acc Thr Gly Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr 465 470 475	1680
gga cgt aag aaa gat ctg atc gtg acc gcg ggc ggc aag aac gtt tcc Gly Arg Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser 480 485 490	1728
cca gga ccc atg gaa gac atc atc cgc gca cac cca ctg gtc agc cag Pro Gly Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln 495 500 505 510	1776
gcc atg gtg gtg ggc gat ggt aaa cca ttc gtt ggc ctg ctg gtg acc Ala Met Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr 515 520 525	1824
ttg gat cca gat atg ttg aag cgg tgg aag ctg aac cac aac att gcg Leu Asp Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala 530 535 540	1872
gaa tcc cgc acg gtt tct gag att gct act gat cct gca ctg cgt gcg Glu Ser Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala 545 550 555	1920
gaa atc cag gat gca gtc aac aac gct aat gcc acg gtg tct cat tca Glu Ile Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser 560 565 570	1968

032301.1181.ST25.txt

gag gcg atc aag cgg ttc tac atc ctt gat cgc gac ctg acc gag gaa 2016
 Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu
 575 580 585 590

gcc gac gag ctg acc cca acg ctg aag gtc aag cgc aac gtt gtt gtt 2064
 Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val
 595 600 605

cgc cgt tac gca gac gcc atc gac cac atc tac aac cga tgagtaacac 2113
 Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
 610 615

agagacccaa tttgattggg atggatcgac atggaccgc accgaagtcg gcgaagcacc 2173

aacacgcttc gctgtgggcg tgatggagga tttgcctac attgcagcca ctggcacgga 2233

cggggatgaa gagttcttta ctttgggctc aaatccgggt ctgacgtttg gtgatccgga 2293

gtggctt 2300

<210> 2
 <211> 619
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2

Met Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr Thr Glu
 1 5 10 15

Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr Ala Leu
 20 25 30

Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser Lys Pro
 35 40 45

Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu
 50 55 60

Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly
 65 70 75 80

Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu
 85 90 95

Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser
 100 105 110

Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala
 115 120 125

Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn
 130 135 140

B1
 Cont

Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser
145 150 155 160

Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu
165 170 175

Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu Arg Ile
180 185 190

His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr Ser Gly
195 200 205

Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His Trp Leu
210 215 220

Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile Ala Met
225 230 235 240

Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val Leu Ala
245 250 255

Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln Ser His
260 265 270

Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser Arg Pro
275 280 285

Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg Asn Ala
290 295 300

Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile Met Phe
305 310 315 320

Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu Asp Thr
325 330 335

Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala Phe Asp
340 345 350

Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp Val Gln
355 360 365

Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu His Phe
370 375 380

Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu Thr Glu
Page 5

B1
cont

385

390

400

Ser Ala Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile Gly Thr
405 410 415

Val Gly Lys Pro Met Gly Gly Met Thr Ile Lys Ile Asn Glu Asp Gly
420 425 430

Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp Asn Asn
435 440 445

Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn Thr Gly
450 455 460

Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr Gly Arg
465 470 475 480

Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser Pro Gly
485 490 495

Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln Ala Met
500 505 510

Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp
515 520 525

Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser
530 535 540

Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile
545 550 555 560

Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala
565 570 575

Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp
580 585 590

Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val Arg Arg
595 600 605

Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
610 615

<210> 3
<211> 24
<212> DNA
<213> Corynebacterium glutamicum

B!
CMT

<400> 3
tgattggtgc agatataaga agtt

24

<210> 4
<211> 17
<212> DNA
<213> Corynebacterium glutamicum

B!
<400> 4
cagcgaagcg tgttggt

17
